(J) 00420   O/PE

ENTERED

Serial Number: _/o/ 02/,753_

CRF Processing Date: _1/22/2002_
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _#3_
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: _Corrected <1407 and <1417 - changed to <1507 and <1517_
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.   3/1/95

OIPE

RAW SEQUENCE LISTING   DATE: 01/22/2002
PATENT APPLICATION: US/10/021,753   TIME: 19:32:27

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\01222002\J021753.raw

```
   3 <110> APPLICANT: FUJISE, KEN
   4        YEH, EDWARD T.H.
   6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO FORTILIN, AN
   7        ANTI-APOPTOTIC MOLECULE, AND MODULATORS OF FORTILIN
   9 <130> FILE REFERENCE: UTSH:251US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/021,753
  12 <141> CURRENT FILING DATE: 2001-10-30
  14 <150> PRIOR APPLICATION NUMBER: 60/244,416
  15 <151> PRIOR FILING DATE: 2000-10-30
  17 <160> NUMBER OF SEQ ID NOS: 9
  19 <170> SOFTWARE: PatentIn Ver. 2.1
  21 <210> SEQ ID NO: 1
  22 <211> LENGTH: 830
  23 <212> TYPE: DNA
  24 <213> ORGANISM: Homo sapiens
  26 <220> FEATURE:
  27 <221> NAME/KEY: CDS
  28 <222> LOCATION: (95)..(613)
  30 <400> SEQUENCE: 1
  31 cccccccgag cgccgctccg gctgcaccgc gctcgctccg agtttcaggc tcgtgctaag 60
  33 ctagcgccgt cgtcgtctcc cttcagtcgc catc atg att atc tac cgg gac ctc 115
  34                                    Met Ile Ile Tyr Arg Asp Leu
  35                                     1               5
  37 atc agc cac gat gag atg ttc tcc gac atc tac aag atc cgg gag atc  163
  38 Ile Ser His Asp Glu Met Phe Ser Asp Ile Tyr Lys Ile Arg Glu Ile
  39         10                  15                  20
  41 gcg gac ggg ttg tgc ctg gag gtg gag ggg aag atg gtc agt agg aca  211
  42 Ala Asp Gly Leu Cys Leu Glu Val Glu Gly Lys Met Val Ser Arg Thr
  43         25                  30                  35
  45 gaa ggt aac att gat gac tcg ctc att ggt gga aat gcc tcc gct gaa  259
  46 Glu Gly Asn Ile Asp Asp Ser Leu Ile Gly Gly Asn Ala Ser Ala Glu
  47  40                  45                  50                  55
  49 ggc ccc gag ggc gaa ggt acc gaa agc aca gta atc act ggt gtc gat  307
  50 Gly Pro Glu Gly Glu Gly Thr Glu Ser Thr Val Ile Thr Gly Val Asp
  51                  60                  65                  70
  53 att gtc atg aac cat cac ctg cag gaa aca agt ttc aca aaa gaa gcc  355
  54 Ile Val Met Asn His His Leu Gln Glu Thr Ser Phe Thr Lys Glu Ala
  55                  75                  80                  85
  57 tac aag aag tac atc aaa gat tac atg aaa tca atc aaa ggg aaa ctt  403
  58 Tyr Lys Lys Tyr Ile Lys Asp Tyr Met Lys Ser Ile Lys Gly Lys Leu
  59         90                  95                 100
  61 gaa gaa cag aga cca gaa aga gta aaa cct ttt atg aca ggg gct gca  451
  62 Glu Glu Gln Arg Pro Glu Arg Val Lys Pro Phe Met Thr Gly Ala Ala
```

```
63      105                    110                    115
65 gaa caa atc aag cac atc ctt gct aat ttc aaa aac tac cag ttc ttt    499
66 Glu Gln Ile Lys His Ile Leu Ala Asn Phe Lys Asn Tyr Gln Phe Phe
67 120              125                    130                    135
69 att ggt gaa aac atg aat cca gat ggc atg gtt gct cta ttg gac tac    547
70 Ile Gly Glu Asn Met Asn Pro Asp Gly Met Val Ala Leu Leu Asp Tyr
71               140                    145                    150
73 cgt gag gat ggt gtg acc cca tat atg att ttc ttt aag gat ggt tta    595
74 Arg Glu Asp Gly Val Thr Pro Tyr Met Ile Phe Phe Lys Asp Gly Leu
75               155                    160                    165
77 gaa atg gaa aaa tgt taa caaatgtggc aattattttg gatctatcac          643
78 Glu Met Glu Lys Cys
79           170
81 ctgtcatcat aactggcttc tgcttgtcat ccacacaaca ccaggactta agacaaatgg 703
83 gactgatgtc atcttgagct cttcatttat tttgactgtg atttatttgg agtggaggca 763
85 ttgttttttaa gaaaaacatg tcatgtaggt tgtctaaaaa taaaatgcat ttaaactcat 823
87 ttgagag                                                            830
90 <210> SEQ ID NO: 2
91 <211> LENGTH: 172
92 <212> TYPE: PRT
93 <213> ORGANISM: Homo sapiens
95 <400> SEQUENCE: 2
96 Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp
97   1             5                    10                    15
98 Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu
99             20                    25                    30
100 Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
101           35                    40                    45
102 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
103       50                    55                    60
104 Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
105   65                    70                    75                    80
106 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
107                   85                    90                    95
108 Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
109               100                   105                   110
110 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
111           115                   120                   125
112 Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
113       130                   135                   140
114 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met
115 145                   150                   155                   160
116 Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
117               165                   170
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 172
123 <212> TYPE: PRT
124 <213> ORGANISM: Rabbit
126 <400> SEQUENCE: 3
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Input Set : A:\PTO.AMC.txt
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```
127 Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp
128  1            5               10            15
130 Ile Tyr Lys Ile Arg Glu Ile Ala Gly Gly Leu Cys Leu Glu Val Glu
131          20              25              30
133 Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
134          35              40              45
136 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
137      50              55              60
139 Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
140  65              70              75              80
142 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
143              85              90              95
145 Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
146              100             105             110
148 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
149          115             120             125
151 Phe Lys Asn Tyr Gln Phe Tyr Ile Gly Glu Asn Met Asn Pro Asp Gly
152      130             135             140
154 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Phe Met
155 145             150             155             160
157 Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
158              165             170
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 172
163 <212> TYPE: PRT
164 <213> ORGANISM: Mus musculus
166 <400> SEQUENCE: 4
167 Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Leu Phe Ser Asp
168  1            5               10            15
170 Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu
171          20              25              30
173 Gly Lys Met Val Ser Arg Thr Glu Gly Ala Ile Asp Asp Ser Leu Ile
174          35              40              45
176 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
177      50              55              60
179 Thr Val Val Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
180  65              70              75              80
182 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
183              85              90              95
185 Lys Ser Leu Lys Gly Lys Leu Glu Glu Gln Lys Pro Glu Arg Val Lys
186              100             105             110
188 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
189          115             120             125
191 Phe Asn Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
192      130             135             140
194 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Phe Met
195 145             150             155             160
197 Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
198              165             170
```

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Output Set: N:\CRF3\01222002\J021753.raw

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201 <210> SEQ ID NO: 5
202 <211> LENGTH: 172
203 <212> TYPE: PRT
204 <213> ORGANISM: Chicken
206 <400> SEQUENCE: 5
207 Met Ile Ile Tyr Arg Asp Cys Ile Ser Gln Asp Glu Met Phe Ser Asp
208  1               5                  10                  15
210 Ile Tyr Lys Ile Arg Glu Val Ala Asn Gly Leu Cys Leu Glu Val Glu
211              20                  25                  30
213 Gly Lys Met Val Thr Arg Thr Glu Gly Gln Ile Asp Asp Ser Leu Ile
214          35                  40                  45
216 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ala
217      50                  55                  60
219 Thr Val Ile Thr Gly Val Asp Ile Val Ile Asn His His Leu Gln Glu
220  65                  70                  75                  80
222 Thr Ser Phe Thr Lys Glu Ser Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
223              85                  90                  95
225 Lys Ala Ile Lys Ala Arg Leu Glu Glu His Lys Pro Glu Arg Val Lys
226              100                 105                 110
228 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
229          115                 120                 125
231 Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
232      130                 135                 140
234 Met Val Ala Leu Leu Asp Phe Arg Glu Asp Gly Val Thr Pro Tyr Met
235 145                 150                 155                 160
237 Ile Phe Phe Lys Asp Gly Leu Glu Ile Glu Lys Cys
238              165                 170
241 <210> SEQ ID NO: 6
242 <211> LENGTH: 172
243 <212> TYPE: PRT
244 <213> ORGANISM: D. Melanogaster
246 <400> SEQUENCE: 6
247 Met Lys Ile Tyr Lys Asp Ile Ile Thr Gly Asp Glu Met Phe Ala Asp
248  1               5                  10                  15
250 Thr Tyr Lys Met Lys Leu Val Asp Asp Val Ile Tyr Glu Val Tyr Gly
251              20                  25                  30
253 Lys Leu Ile Thr Arg Gln Gly Asp Asp Ile Lys Leu Glu Gly Ala Asn
254          35                  40                  45
256 Ala Ser Ala Glu Glu Ala Asp Glu Gly Thr Asp Ile Thr Ser Glu Ser
257      50                  55                  60
259 Gly Val Asp Val Val Leu Asn His Arg Leu Thr Glu Cys Phe Ala Phe
260  65                  70                  75                  80
262 Gly Asp Lys Lys Ser Tyr Thr Leu Tyr Leu Lys Asp Tyr Met Lys Lys
263              85                  90                  95
265 Val Leu Ala Lys Leu Glu Glu Lys Ser Pro Asp Gln Val Asp Ile Phe
266          100                 105                 110
268 Lys Thr Asn Met Asn Lys Ala Met Lys Asp Ile Leu Gly Arg Phe Lys
269          115                 120                 125
271 Glu Leu Gln Phe Phe Thr Gly Glu Ser Met Asp Cys Asp Gly Met Val
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Input Set : A:\PTO.AMC.txt
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```
272     130                    135                  140
274 Ala Leu Val Glu Tyr Arg Glu Ile Asn Gly Asp Ser Val Pro Val Leu
275 145                   150               155                  160
277 Met Phe Phe Lys His Gly Leu Glu Glu Glu Lys Cys
278                  165                    170
281 <210> SEQ ID NO: 7
282 <211> LENGTH: 181
283 <212> TYPE: PRT
284 <213> ORGANISM: C. ELEGANS
286 <400> SEQUENCE: 7
287 Met Leu Ile Tyr Lys Asp Ile Ile Ser Asp Asp Glu Leu Ser Ser Asp
288  1                   5                  10                  15
290 Ser Phe Pro Met Lys Leu Val Asp Asp Leu Val Tyr Glu Phe Lys Gly
291             20                    25                  30
293 Lys His Val Val Arg Lys Glu Gly Glu Ile Val Leu Ala Gly Ser Asn
294         35                    40                  45
296 Pro Ser Ala Glu Glu Gly Ala Glu Asp Asp Gly Ser Asp Glu His Val
297      50                    55                  60
299 Glu Arg Gly Ile Asp Ile Val Leu Asn His Lys Leu Val Glu Met Asn
300  65                   70                  75                  80
302 Cys Tyr Glu Asp Ala Ser Met Phe Lys Ala Tyr Ile Lys Lys Phe Met
303             85                    90                  95
305 Lys Asn Val Ile Asp His Met Glu Lys Asn Asn Arg Asp Lys Ala Asp
306             100                   105                 110
308 Val Asp Ala Phe Lys Lys Lys Ile Gln Gly Trp Val Val Ser Leu Leu
309             115                   120                 125
311 Ala Lys Asp Arg Phe Lys Asn Leu Ala Phe Phe Ile Gly Glu Arg Ala
312      130                   135                 140
314 Ala Glu Gly Ala Glu Asn Gly Gln Val Ala Ile Ile Glu Tyr Arg Asp
315 145                   150               155                  160
317 Val Asp Gly Thr Glu Val Pro Thr Leu Met Leu Val Lys Glu Ala Ile
318             165                   170                 175
320 Ile Glu Glu Lys Cys
321             180
324 <210> SEQ ID NO: 8
325 <211> LENGTH: 166
326 <212> TYPE: PRT
327 <213> ORGANISM: S. Cerevisiae
329 <400> SEQUENCE: 8
330 Met Ile Ile Tyr Lys Asp Ile Phe Ser Asn Asp Glu Leu Leu Ser Asp
331  1                   5                  10                  15
333 Ala Tyr Asp Ala Lys Leu Val Asp Asp Val Ile Tyr Glu Ala Asp Cys
334             20                    25                  30
336 Ala Met Val Asn Val Gly Gly Asp Asn Ile Asp Ile Gly Ala Asn Pro
337         35                    40                  45
339 Ser Ala Glu Gly Gly Asp Asp Asp Val Glu Glu Gly Ala Glu Met Val
340      50                    55                  60
342 Asn Asn Val Val His Ser Phe Arg Leu Gln Gln Thr Ala Phe Asp Lys
343  65                   70                  75                  80
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/021,753

DATE: 01/22/2002
TIME: 19:32:28

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\01222002\J021753.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number